

# Package ‘rbi’

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**Title** R Interface to LibBi

**Imports** data.table, ncd4, processx, reshape2

**Suggests** coda, covr (>= 3.2.0), R.rsp, stringi, testthat, ggplot2

**Description** Provides a complete R interface to LibBi, a library for Bayesian inference (see <<http://libbi.org>> and <[doi:10.18637/jss.v067.i10](https://doi.org/10.18637/jss.v067.i10)> for more information). This includes functions for manipulating LibBi models, for reading and writing LibBi input/output files, for converting LibBi output to provide traces for use with the coda package, and for running LibBi from R.

**License** GPL-3

**URL** <https://github.com/sbfnk/RBi>

**BugReports** <https://github.com/sbfnk/RBi/issues>

**SystemRequirements** LibBi (>= 1.4.2)

**LazyLoad** no

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**VignetteBuilder** R.rsp

**NeedsCompilation** no

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rbi-package	<i>RBi - R interface for libbi</i>
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## Description

rbi is an interface to libbi, a library for Bayesian Inference

## Details

The package includes a wrapper for the libbi script, allowing to launch the libbi command from within R. It also provides various utility functions to browse the output from libbi, for instance to plot the results.

The package is made of various components:

- A wrapper around libbi called `libbi`.
- A `bi_model` class that can be used to load and manipulate libbi models
- Functions to manipulate the results of the libbi command, which are stored in NetCDF files. Those functions allow to extract variables of interest.

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## References

<http://libbi.org/>

## See Also

[libbi](#)

## Examples

```
example_output_file <- system.file(package="rbi", "example_output.nc")
bi_file_summary(example_output_file)
mu_sigma <- bi_read(example_output_file, c("mu", "sigma"))
bi_write("mu_sigma.nc", mu_sigma)

## examples for running libbi from rbi (will take a few minutes)
## Not run: demo(PZ_generate_dataset)
## Not run: demo(PZ_PMMH)
```

```
## Not run: demo(PZ_SMC2)
## Not run: demo(PZ_filtering)
```

---

add_block	<i>Add a block to a LibBi model</i>
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---

### Description

Add a block to a LibBi model. If that block exists, it will be removed first.

### Usage

```
## S3 method for class 'bi_model'
add_block(x, name, lines, options, ...)
```

### Arguments

x	a <code>bi_model</code> object
name	name of the block
lines	character vector, lines in the block
options	any options to the block
...	ignored

### Value

a `bi_model` object containing the new block

---

attach_data	<i>Attach a new file or data set to a libbi object</i>
-------------	--

---

### Description

Adds an (output, obs, etc.) file to a `libbi` object. This is useful to recreate a `libbi` object from the model and output files of a previous run

The `bi_write` options `append` and `overwrite` determine what exactly the file will contain at the end of this. If they are both `FALSE` (the default), any existing file will be ignored. If `append` is `TRUE`, the existing data in the file will be preserved, and any data set passed as `data` and not already in the file will be added. If `overwrite` is `TRUE`, existing data in the file will be preserved except for variables that exist in the passed data.

**Usage**

```
## S3 method for class 'libbi'
attach_data(x, file, data, in_place = FALSE,
            append = FALSE, overwrite = FALSE, quiet = FALSE,
            time_dim = character(0), coord_dims = list(), ...)
```

**Arguments**

x	a <a href="#">libbi</a> object
file	the type of the file to attach, one of "output", "obs", "input" or "init"
data	name of the file to attach, or a list of data frames that contain the outputs; it will be assumed that this is already thinned
in_place	if TRUE, replace the file in place if it already exists in the libbi object; this can speed up the operation if append=TRUE as otherwise the file will have to be read and used again; it should be used with care, though, as it can render existing <a href="#">libbi</a> objects invalid as the files they are pointing to are changed.
append	if TRUE, will append variables if file exists; default: FALSE
overwrite	if TRUE, will overwrite variables if file exists; default: FALSE
quiet	if TRUE, will suppress the warning message normally given if replace=TRUE and the file exists already
time_dim	the name of the time dimension, if one exists; default: "time"
coord_dims	the names of the coordinate dimension, if any; should be a named list of character vectors, they are matched to variables names
...	any options to <a href="#">bi_write</a> (e.g., 'time_dim')

**Examples**

```
bi <- libbi(model = system.file(package="rbi", "PZ.bi"))
example_output <- bi_read(system.file(package="rbi", "example_output.nc"))
bi <- attach_data(bi, "output", example_output)
```

---

bi\_contents

*Bi contents*


---

**Description**

This function gets the name of all the variables in the passed file, list or [libbi](#) object

**Usage**

```
bi_contents(read, ...)
```

**Arguments**

read            either a path to a NetCDF file, or a NetCDF connection created using `nc_open`,  
or a `libbi` object from which to read the output

...            any parameters for `bi_open` (especially "file")

**Value**

vector of variable names

**Examples**

```
example_output_file <- system.file(package="rbi", "example_output.nc")
bi_contents(example_output_file)
```

---

bi_dim_len	<i>NetCDF dimension length</i>
------------	--------------------------------

---

**Description**

This function returns the length of a dimension in a NetCDF file.

**Usage**

```
bi_dim_len(filename, dim)
```

**Arguments**

filename        path to a NetCDF file

dim            name of the dimension to check

**Value**

dimension length

---

bi_file_summary	<i>NetCDF File Summary</i>
-----------------	----------------------------

---

### Description

This function prints a little summary of the content of a NetCDF file, as well as its creation time. You can then retrieve variables of interest using [bi\\_read](#).

### Usage

```
bi_file_summary(...)
```

### Arguments

... Any extra parameters to [bi\\_open](#), especially `x` and `file`

### Value

None

### Examples

```
example_output_file <- system.file(package="rbi", "example_output.nc")
bi_file_summary(example_output_file)
```

---

bi_generate_dataset	<i>Bi Generate Dataset</i>
---------------------	----------------------------

---

### Description

This is a wrapper around `libbi sample --target joint --nsamples 1`, to generate a synthetic dataset from a model. Parameters can be passed via the `'init'` option (see [run.libbi](#), otherwise they are generated from the prior specified in the model. The end time should be specified using the `"end_time"` option. If this is not given, only a parameter set is sampled. Use the `'noutputs'` or `'output_every'` options to control the number of data points being generated. By default, `output_every` is set to 1.

### Usage

```
bi_generate_dataset(..., output_every = 1)
```

### Arguments

... arguments to be passed to [sample.libbi](#), especially `'model'`, `'end_time'` and `'seed'`.

`output_every` real; if given, `noutputs` will be set so that there is output every `output_every` time steps; if set to 0, only generate an output at the final time

**Value**

generated data set

---

bi_model	<i>Bi Model</i>
----------	-----------------

---

**Description**

bi\_model creates a model object for Rbi from a libbi file, URL or character vector. Once the instance is created, the model can be fed to a [libbi](#) object.

**Usage**

```
bi_model(filename, lines, ...)
```

**Arguments**

filename	the file name of the model file
lines	lines of the model (if no filename is given), a character vector
...	ignored

**See Also**

[fix](#), [insert\\_lines](#), [remove\\_lines](#), [replace\\_all](#), [get\\_name](#), [set\\_name](#), [write\\_model](#)

**Examples**

```
model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
```

---

bi_open	<i>Bi open</i>
---------	----------------

---

**Description**

This function opens an NetCDF file The file can be specified as a string to the filepath, in which case a NetCDF connection is opened, or directly as a NetCDF connection.

**Usage**

```
bi_open(x, file = "output")
```



**Arguments**

x	either a path to a NetCDF file, or a NetCDF connection created using <code>nc_open</code> , or a <code>libbi</code> object from which to read the output
file	file to open (out of "input", "init", "obs", "output"), if x is given as a <code>libbi</code> object; by default, will read output file

**Value**

open NetCDF connection

---

bi_read	<i>Bi Read</i>
---------	----------------

---

**Description**

This function reads all variable from a NetCDF file or the output of a `libbi` object. The file can be specified as a string to the filepath, in which case a NetCDF connection is opened, or directly as a NetCDF connection.

**Usage**

```
bi_read(x, vars, dims, model, type, file, missval_threshold,
        coord_dims = list(), vector, thin, verbose = FALSE,
        clear_cache = FALSE, init_to_param = FALSE, burn = 0,
        missval.threshold, init.to.param = FALSE)
```

**Arguments**

x	either a path to a NetCDF file, or a NetCDF connection created using <code>nc_open</code> , or a <code>libbi</code> object from which to read the output
vars	variables to read; if not given, all will be read
dims	factors for dimensions
model	model file or a <code>bi_model</code> object (if x is not a <code>libbi</code> object)
type	vector of types of variable to read (out of "param", "state", "noise", "obs"). This needs 'x' to be a <code>libbi</code> object or model to be specified
file	which file to read (if x is given as a <code>libbi</code> object): one of "output" (default), "init", "input", "obs"
missval_threshold	upper threshold for the likelihood
coord_dims	any coord dimensions, given as a named list of character vectors, where each element corresponds to the variable of the same name, and the character vector are the coord dimensions
vector	deprecated; if TRUE, will return results as vectors, not data.frames
thin	thinning (keep only 1/thin of samples)

verbose	if TRUE, will print variables as they are read
clear_cache	if TRUE, will clear the cache and re-read the file even if cached data exists
init_to_param	logical; if TRUE, convert states to initial values
burn	number of initial samples to discard; default: 0
missval.threshold	deprecated; use missval_threshold instead
init.to.param	deprecated; use init_to_param instead

**Value**

list of data frames and/or numbers

**Examples**

```
example_output_file <- system.file(package="rbi", "example_output.nc")
d <- bi_read(example_output_file)
```

---

bi_write	<i>Create (e.g., init or observation) files for LibBi</i>
----------	---

---

**Description**

This function creates (or appends to) a NetCDF file for LibBi from the given list of vectors and/or data frames. Since any files can be passed to `libbi` directly via the `init`, `input` and `obs` options, this is mostly used internally, this is mostly used internally.

**Usage**

```
bi_write(filename, variables, timed, append = FALSE, overwrite = FALSE,
         time_dim, coord_dims, dim_factors, value_column = "value",
         guess_time = FALSE, guess_coord = FALSE, verbose)
```

**Arguments**

filename	a path to a NetCDF file to write the variables into, which will be overwritten if it already exists. If necessary, ".nc" will be added to the file name
variables	a list object, the names of which should be the variable names and values should be either single values or data frames
timed	deprecated; timed variables should be given as data frames
append	if TRUE, will append variables if file exists; default: FALSE
overwrite	if TRUE, will overwrite variables if file exists; default: FALSE
time_dim	the name of the time dimension, if one exists; default: "time"
coord_dims	the names of the coordinate dimension, if any; should be a named list of character vectors, they are matched to variables names

dim_factors	factors that dimensions have; this corresponds to the dims element of a <a href="#">libbi</a> object
value_column	if any variables are data frames, which column contains the values (default: "value")
guess_time	whether to guess time dimension; this would be a numerical column in the data frame given which is not the value_column; only one such column must exist
guess_coord	whether to guess the coordinate dimension; this would be a column with varying value which is not the time or value column
verbose	if TRUE, will print variables as they are read

### Details

The list of variables must follow the following rules. Each element of the list must itself be one of:

- 1) a data frame with a value\_column column (see option 'value\_column') and any number of other columns indicating one or more dimensions
- 2) a numeric vector of length one, with no dimensions

The name of the list elements itself is used to create the corresponding variable in the NetCDF file.

### Value

A list of the time and coord dims, and factors in extra dimensions, if any

### Examples

```
filename <- tempfile(pattern="dummy", fileext=".nc")
a <- 3
b <- data.frame(dim_a = rep(1:3, time = 2), dim_b = rep(1:2, each = 3), value = 1:6)
variables <- list(a=a, b=b)
bi_write(filename, variables)
bi_file_summary(filename)
```

---

enable_outputs	<i>Enable outputting variables in a <a href="#">bi_model</a></i>
----------------	--

---

### Description

Any variable type given will have any 'has\_output=0' option removed in the given model..

### Usage

```
enable_outputs(x, type = "all")
```

### Arguments

x	a <a href="#">bi_model</a> object
type	either "all" (default), or a vector of variable types that are to have outputs enabled

**Value**

a bi model object of the new model

**See Also**

[bi\\_model](#)

**Examples**

```
model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
PZ[6] <- "param mu (has_output=0)"
PZ <- enable_outputs(PZ)
```

---

Equals.bi_model	<i>Check if two models are equal</i>
-----------------	--------------------------------------

---

**Description**

Ignores differences in the model name.

**Usage**

```
## S3 method for class 'bi_model'
e1 == e2, ...
```

**Arguments**

e1	a <a href="#">bi_model</a>
e2	a <a href="#">bi_model</a>
...	ignored

**Value**

value TRUE or FALSE

**Examples**

```
model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
PZ == PZ # TRUE
```

---

Extract.bi_model	<i>Subset model lines</i>
------------------	---------------------------

---

**Description**

Extracts a subset of lines from the model.

**Usage**

```
## S3 method for class 'bi_model'
x[i, ...]
```

**Arguments**

x	A bi_model
i	A vector of line numbers
...	ignored

**Examples**

```
model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
PZ[3:4]
```

---

Extract_assign.bi_model	<i>Subset and replace model lines</i>
-------------------------	---------------------------------------

---

**Description**

Extracts a subset of lines from the model and assigns new character strings.

**Usage**

```
## S3 replacement method for class 'bi_model'
x[i, ...] <- value
```

**Arguments**

x	A bi_model
i	A vector of line numbers
...	ignored
value	A vector of the same length as i, containing the replacement strings

**Examples**

```

model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
PZ[3:4] <- c("const e = 0.4", "const m_l = 0.05")

```

---

extract_sample	<i>Extract a sample from a LibBi run.</i>
----------------	---

---

**Description**

This function takes the provided [libbi](#) results and extracts a data frame.

**Usage**

```
extract_sample(x, np, ...)
```

**Arguments**

x	a <a href="#">libbi</a> object which has been run, or a list of data frames containing parameter traces (as returned by <code>from bi_read</code> )
np	iteration to extract; if set to "last", the last sample will be extracted. If not given a random sample will be extracted
...	parameters to <code>bi_read</code> (e.g., dimensions)

**Value**

list of parameters and trajectories

---

filter	<i>Using the LibBi wrapper to filter</i>
--------	--

---

**Description**

The method `filter` launches `libbi` to filter state trajectories. See the options to `run.libbi` for how to specify the various components of sampling with LibBi, and the LibBi manual for all options that can be passed when the client is `filter`.

If `x` is given as a `'bi_model'`, a `libbi` object will be created from the model For the help page of the base R `filter` function, see [filter](#).

**Usage**

```

## S3 method for class 'libbi'
filter(x, ...)

## S3 method for class 'bi_model'
filter(x, ...)

```

**Arguments**

`x` a `libbi` or `bi_model` object, or the name of a file containing the model  
`...` options to be passed to `run.libbi`

**Value**

a `libbi` object

---

<code>fix</code>	<i>Fix noise term, state or parameter of a libbi model</i>
------------------	--

---

**Description**

Replaces all variables with fixed values as given ; note that this will not replace differential equations and lead to an error if applied to states that are changed inside an "ode" block

For the help page of the base R `fix` function, see [fix](#).

**Usage**

```
## S3 method for class 'bi_model'
fix(x, ...)
```

**Arguments**

`x` a `bi_model` object  
`...` values to be assigned to the (named) variables

**Value**

a bi model object of the new model

**See Also**

[bi\\_model](#)

**Examples**

```
model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
PZ <- fix(PZ, alpha = 0)
```

---

flatten	<i>Flatten list of data frames This function takes a list of data frames (such as, for example, returned by <a href="#">bi_read</a>) and converts it to a flat data frame</i>
---------	---

---

**Description**

Flatten list of data frames This function takes a list of data frames (such as, for example, returned by [bi\\_read](#)) and converts it to a flat data frame

**Usage**

```
flatten(x)
```

**Arguments**

x	The list of data frames
---	-------------------------

---

get_block	<i>Get the contents of a block in a LibBi model</i>
-----------	---

---

**Description**

Returns the contents of a block in a LibBi model as a character vector of lines.

**Usage**

```
## S3 method for class 'bi_model'
get_block(x, name, shell = FALSE, ...)
```

**Arguments**

x	a <a href="#">bi_model</a> object
name	name of the block
shell	if TRUE (default:FALSE), will return the shell (i.e., the definition of the block) as well as content; this is useful, e.g., to see options passed to a transition or ode block
...	ignored

**Value**

a character vector of the lines in the block



---

get_const	<i>Get constants in a LibBi model</i>
-----------	---------------------------------------

---

**Description**

Get constants contained in a LibBi model and their values. This will attempt to evaluate any calculation on the right hand side. Failing that, it will be returned verbatim.

**Usage**

```
get_const(model)
```

**Arguments**

model            a `bi_model` object

**Value**

list of constants (as names) and their values

---

get_dims	<i>Get dimensions in a LibBi model</i>
----------	--

---

**Description**

Get dimensions contained in a LibBi model and their sizes

**Usage**

```
get_dims(model, type)
```

**Arguments**

model            a `bi_model` object  
type            a character vector of one or more types

**Value**

list of dimensions (as names) and their sizes

---

get_name	<i>Get the name of a bi model</i>
----------	-----------------------------------

---

### Description

Extracts the name of a bi model (first line of the .bi file).

### Usage

```
## S3 method for class 'bi_model'  
get_name(x, ...)
```

### Arguments

x	a <a href="#">bi_model</a> object
...	ignored

### Value

the name of the model

### See Also

[bi\\_model](#)

### Examples

```
model_file_name <- system.file(package="rbi", "PZ.bi")  
PZ <- bi_model(filename = model_file_name)  
get_name(PZ)
```

---

get_traces	<i>Get the parameter traces</i>
------------	---------------------------------

---

### Description

This function takes the provided [libbi](#) object which has been run and returns a data frame with the parameter traces.

### Usage

```
get_traces(x, model, burnin, all = FALSE, ...)
```

**Arguments**

x	a <code>libbi</code> object which has been run, or a list of data frames containing parameter traces (as returned by <code>bi_read</code> ); if it is not a <code>libbi</code> object, either 'all' must be TRUE or a model given
model	a model to get the parameter names from; not needed if 'run' is given as a <code>libbi</code> object or 'all' is set to TRUE
burnin	proportion of iterations to discard as burn-in (if between 0 and 1), or number of samples to discard (if >1)
all	whether all variables in the run file should be considered (otherwise, just parameters)
...	parameters to <code>bi_read</code> (e.g., dimensions)

**Value**

data frame with parameter traces; this can be fed to coda routines

---

insert_lines	<i>Insert lines in a LibBi model</i>
--------------	--------------------------------------

---

**Description**

Inserts one or more lines into a `libbi` model. If one of `before` or `after` is given, the line(s) will be inserted before or after a given line number or block name, respectively. If one of `at_beginning_of` or `at_end_of` is given, the lines will be inserted at the beginning/end of the block, respectively.

**Usage**

```
## S3 method for class 'bi_model'
insert_lines(x, lines, before, after, at_beginning_of,
            at_end_of, ...)
```

**Arguments**

x	a <code>bi_model</code> object
lines	vector or line(s)
before	line number before which to insert line(s)
after	line number after which to insert line(s)
at_beginning_of	block at the beginning of which to insert lines(s)
at_end_of	block at the end of which to insert lines(s)
...	ignored

**Value**

the updated `bi` model

**See Also**[bi\\_model](#)**Examples**

```

model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
PZ <- insert_lines(PZ, lines = "noise beta", after = 8)

```

---

join	<i>Join multiple <a href="#">libbi</a> objects</i>
------	--

---

**Description**

This function can be used to join multiple [libbi](#) objects into one (e.g., parallel MCMC runs into one long chain)

**Usage**

```

## S3 method for class 'libbi'
join(x, ...)

```

**Arguments**

x	a <a href="#">libbi</a> object
...	ignored

---

libbi	<i>LibBi Wrapper</i>
-------	----------------------

---

**Description**

[libbi](#) allows to call LibBi. Upon creating a new [libbi](#) object, the following arguments can be given. Once the instance is created, LibBi can be run through the [sample](#), [filter](#), or [optimise](#), or [rewrite](#) methods. Note that [libbi](#) objects can be plotted using [plot](#) if the `rbi.helpers` package is loaded.

**Usage**

```

libbi(model, path_to_libbi, dims, use_cache = TRUE, ...)

```

**Arguments**

model	either a character vector giving the path to a model file (typically ending in ".bi"), or a bi_model object
path_to_libbi	path to LibBi binary; by default it tries to locate the libbi binary using the which Unix command, after having loaded "~/.bashrc" if present; if unsuccessful it tries "~/PathToBiBin/libbi"; if unsuccessful again it fails.
dims	any named dimensions, as list of character vectors
use_cache	logical; whether to use the cache (default: true)
...	options passed to <code>run.libbi</code>

**Value**

a `libbi` object

**See Also**

[sample](#), [filter](#), [optimise](#), [rewrite](#)

**Examples**

```
bi_object <- libbi(model = system.file(package="rbi", "PZ.bi"))
```

---

logLik

*Using the LibBi wrapper to logLik*


---

**Description**

The method `logLik` extracts the log-likelihood of a `libbi` object. This can be done, for example, after a call to [sample](#) to inspect the chain log-likelihoods.

For the help page of the base R `logLik` function, see [logLik](#).

**Usage**

```
## S3 method for class 'libbi'
logLik(object, ...)
```

**Arguments**

object	a <code>libbi</code> object
...	options to be passed to <code>run.libbi</code>

**Value**

a vector of log-likelihood

---

optimise	<i>Using the LibBi wrapper to optimise</i>
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---

### Description

The method `optimise` launches `libbi` to optimise the parameters with respect to the likelihood or posterior distribution. See the options to `run.libbi` for how to specify the various components of sampling with LibBi, and the LibBi manual for all options that can be passed when the client is `optimise`.

If `x` is given as a `'bi_model'`, a `libbi` object will be created from the model. For the help page of the base R `optimise` function, see `optimise`.

### Usage

```
## S3 method for class 'libbi'
optimise(x, ...)

## S3 method for class 'bi_model'
optimise(x, ...)
```

### Arguments

<code>x</code>	a <code>libbi</code> or <code>link{bi_model}</code> object, or the name of a file containing the model
<code>...</code>	options to be passed to <code>run.libbi</code>

### Value

a `libbi` object

---

option_list	<i>Convert string to option list</i>
-------------	--------------------------------------

---

### Description

This function is used to convert an option string into a list of options. If a list is given, it will be kept as is.

### Usage

```
option_list(...)
```

### Arguments

<code>...</code>	any number of strings to convert
------------------	----------------------------------

**Value**

option list

---

option_string	<i>Convert Options</i>
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---

**Description**

This function is used to convert a list of options into an options string. If a string is given, it will be taken as such.

**Usage**

```
option_string(...)
```

**Arguments**

... any number of lists of options, or strings (which will be left unmodified). If lists are given, later arguments will override earlier ones

---

predict	<i>Using the LibBi wrapper to predict</i>
---------	---

---

**Description**

The method `predict` is an alias for `sample(target="prediction")`. Usually, an `init` object or file should be given containing posterior samples.

For the help page of the base R `optimise` function, see [optimise](#).

**Usage**

```
## S3 method for class 'libbi'
predict(x, ...)
```

**Arguments**

x a `libbi` object

... any arguments to be passed to [sample](#)

---

print_log	<i>Print the log file a libbi object</i>
-----------	--

---

**Description**

This is useful for diagnosis after a `libbi` run

**Usage**

```
print_log(x)
```

**Arguments**

`x` a `libbi` object, or the name of the log file of a `libbi` run.

---

read_libbi	<i>Read results of a LibBi run from an RDS file or from a folder. This completely reconstructs the saved LibBi object</i>
------------	---

---

**Description**

This reads all options, files and outputs of a LibBi run from a specified RDS file or folder (if `split = TRUE` has been used with `save_libbi`).

**Usage**

```
read_libbi(name, ...)
```

**Arguments**

`name` name of the RDS file(s) to read  
`...` any extra options to pass to `libbi` when creating the new object

**Value**

a `libbi` object



---

remove_lines	<i>Remove line(s) and/or block(s) in a libbi model</i>
--------------	--

---

## Description

Removes one or more lines in a libbi model.

## Usage

```
## S3 method for class 'bi_model'  
remove_lines(x, what, only, type = c("all",  
  "assignment", "sample"), preserve_shell = FALSE, ...)
```

## Arguments

x	a <a href="#">bi_model</a> object
what	either a vector of line number(s) to remove, or a vector of blocks to remove (e.g., "parameter")
only	only remove lines assigning given names (as a vector of character strings)
type	which types of lines to remove, either "all", "sample" (i.e., lines with a "~") or "assignment" (lines with a "<-" or "=") (default: "all")
preserve_shell	if TRUE (default: FALSE), preserve the definition of a block even if all lines are removed; this is useful to preserve options passed to a transition or ode block
...	ignored

## Value

the updated bi model

## See Also

[bi\\_model](#)

## Examples

```
model_file_name <- system.file(package="rbi", "PZ.bi")  
PZ <- bi_model(filename = model_file_name)  
PZ <- remove_lines(PZ, 2)
```

---

remove_vars	<i>Remove variables</i>
-------------	-------------------------

---

**Description**

Removes variables from the left-hand side of a model

Used by [fix](#) and [to\\_input](#)

**Usage**

```
remove_vars(x, vars)
```

**Arguments**

x	a <a href="#">bi_model</a> object
vars	vector of variables to remove
...	values to be assigned to the (named) variables

**Value**

a bi model object of the new model

**See Also**

[bi\\_model](#)

---

replace_all	<i>Replace all instances of a string with another in a model</i>
-------------	--

---

**Description**

Takes every occurrence of one string and replaces it with another

**Usage**

```
## S3 method for class 'bi_model'
replace_all(x, from, to, ...)
```

**Arguments**

x	a <a href="#">bi_model</a> object
from	string to be replaced (a regular expression)
to	new string (which can refer to the regular expression given as from)
...	ignored

**Value**

the updated bi model

**See Also**

[bi\\_model](#)

---

 rewrite

*Using the LibBi wrapper to rewrite*


---

**Description**

The method `rewrite` launches LibBi to rewrite a model to inspect its internal representation in LibBi

If `x` is given as a `'bi_model'`, a `libbi` object will be created from the model

**Usage**

```
## S3 method for class 'libbi'
rewrite(x, ...)
```

```
## S3 method for class 'bi_model'
rewrite(x, ...)
```

**Arguments**

`x` a `libbi` or `bi_model` object, or the name of a file containing the model  
`...` options to be passed to `run.libbi`

**Value**

a `bi_model` object

---

 run

*Using the LibBi wrapper to launch LibBi*


---

**Description**

The method `run` launches LibBi with a particular set of command line `#'` arguments. Normally, this function would not be run by the user, but instead one of the client functions `sample`, `filter`, or `optimise`, or `rewrite`, which pass any options on to `run`. Note that any options specified here are stored in the `libbi` object and do not have to be specified again if another command is run on the object.

**Usage**

```
## S3 method for class 'libbi'
run(x, client, proposal = c("model", "prior"), model,
    fix, options, config, log_file_name = character(0), init, input, obs,
    time_dim = character(0), coord_dims = list(), working_folder,
    output_all = FALSE, sample_obs = FALSE, thin, output_every,
    chain = TRUE, seed = TRUE, debug = FALSE, ...)
```

**Arguments**

<code>x</code>	a <code>libbi</code> object; if this is not given, an empty <code>libbi</code> object will be created
<code>client</code>	client to pass to <code>LibBi</code>
<code>proposal</code>	proposal distribution to use; either "model" (default: proposal distribution in the model) or "prior" (propose from the prior distribution)
<code>model</code>	either a character vector giving the path to a model file (typically ending in ".bi"), or a <code>bi_model</code> object; by default, will use any model given in <code>x</code>
<code>fix</code>	any variable to fix, as a named vector
<code>options</code>	deprecated; pass options directly, see documentation for ...
<code>config</code>	path to a configuration file, containing multiple arguments
<code>log_file_name</code>	path to a file to text file to report the output of <code>LibBi</code> ; if set to an empty vector ( <code>character(0)</code> ) or an empty string (""), which is the default, a temporary log file will be generated
<code>init</code>	initialisation of the model, either supplied as a list of values and/or data frames, or a (netcdf) file name, or a <code>libbi</code> object which has been run (in which case the output of that run is used). If the object given as <code>x</code> has been run before, it will be used here with <code>init-np</code> set to the last iteration of the previous run, unless <code>init</code> is given explicitly.
<code>input</code>	input of the model, either supplied as a list of values and/or data frames, or a (netcdf) file name, or a <code>libbi</code> object which has been run (in which case the output of that run is used as input)
<code>obs</code>	observations of the model, either supplied as a list of values and/or data frames, or a (netcdf) file name, or a <code>libbi</code> object which has been run (in which case the output of that run is used as observations)
<code>time_dim</code>	The time dimension in any R objects that have been passed ( <code>init</code> , <code>input</code> ) and <code>obs</code> ); if <code>NULL</code> (default), will be guessed from the given observation
<code>coord_dims</code>	The coord dimension(s) in any <code>obs</code> R objects that have been passed; if <code>NULL</code> (default), will be guessed from the given observation file given
<code>working_folder</code>	path to a folder from which to run <code>LibBi</code> ; default to a temporary folder.
<code>output_all</code>	deprecated; if set to <code>TRUE</code> , all parameters, states and observations will be saved; good for debugging
<code>sample_obs</code>	deprecated; if set to <code>TRUE</code> , will sample observations
<code>thin</code>	any thinning of MCMC chains (1 means all will be kept, 2 skips every other sample etc.); note that <code>LibBi</code> itself will write all data to the disk. Only when the results are read in with <code>bi_read</code> will thinning be applied.

output_every	real; if given, noutputs will be set so that there is output every output_every time steps; if set to 0, only generate an output at the final time
chain	logical; if set to TRUE and x has been run before, the previous output file will be used as init file, and init-np will be set to the last iteration of the previous run (unless target=="prediction"). This is useful for running inference chains.
seed	Either a number (the seed to supply to LibBi), or a logical variable: TRUE if a seed is to be generated for RBi, FALSE if LibBi is to generate its own seed
debug	logical; if TRUE, print more verbose messages and write all variables to the output file, irrespective of their setting of 'has_output'
...	list of additional arguments to pass to the call to LibBi. Any arguments starting with 'enable'/'disable' can be specified as boolean (e.g., 'assert=TRUE' or 'cuda=TRUE'). Any 'dry-' options can be specified with a "'dry'" argument, e.g., 'dry="parse"'. Any options that would be specified with 'with'/'without' can be specified as character vector to an option named 'with'/'without', respectively, e.g. with="transform-obs-to-state".

**Value**

a `libbi` object, except if `client` is 'rewrite', in which case a `bi_model` object will be returned

**See Also**

`libbi`

**Examples**

```
bi_object <- libbi(model = system.file(package="rbi", "PZ.bi"))
## Not run:
  run(bi_object, client="sample", target="prior")
  bi_file_summary(bi_object)

## End(Not run)
```

---

sample

*Using the LibBi wrapper to sample*

---

**Description**

The method `sample` launches `libbi` to sample from a (prior, posterior or joint) distribution. See the options to `run.libbi` for how to specify the various components of sampling with LibBi, and the LibBi manual for all options that can be passed when the client is `sample`.

If `x` is given as a 'bi\_model', a `libbi` object will be created from the model For the help page of the base R `sample` function, see `sample`.

**Usage**

```
## S3 method for class 'libbi'  
sample(x, ...)  
  
## S3 method for class 'bi_model'  
sample(x, ...)
```

**Arguments**

x                    a `libbi` or `bi_model` object, or the name of a file containing the model  
...                   options to be passed to `run.libbi`

**Value**

a `libbi` object

---

sample\_obs

*Sample observations from a LibBi model that has been run*

---

**Description**

Sample observations from a LibBi model that has been run

**Usage**

```
sample_obs(x, ...)
```

**Arguments**

x                    a `libbi` object  
...                   any options to pass to LibBi

**Value**

the original `libbi` object with added variables in the output file for sampled observations

**Author(s)**

Sebastian Funk

---

save_libbi	<i>Write results of a LibBi run to an RDS file</i>
------------	--

---

**Description**

This saves all options, files and outputs of a LibBi run to an RDS file specified

**Usage**

```
## S3 method for class 'libbi'
save_libbi(x, name, supplement, split = FALSE, ...)
```

**Arguments**

x	a <a href="#">libbi</a> object
name	name of the RDS file(s) to save to. If <code>split=TRUE</code> , this will be taken as a base for the names of the files to be created, e.g. 'dir/name.rds' to create files of the form name_...rds in directory 'dir'.
supplement	any supplementary data to save
split	Logical, defaults to FALSE. Should the objects from the LibBi run be saved separately in a folder.
...	any options to <a href="#">saveRDS</a>

---

set_name	<i>Set the name of a bi model</i>
----------	-----------------------------------

---

**Description**

Changes the name of a bi model (first line of the .bi file) to the specified name.

**Usage**

```
## S3 method for class 'bi_model'
set_name(x, name, ...)
```

**Arguments**

x	a <a href="#">bi_model</a> object
name	Name of the model
...	ignored

**Value**

the updated bi model

**See Also**[bi\\_model](#)**Examples**

```
model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
PZ <- set_name(PZ, "new_PZ")
```

---

`simulate`*Using the LibBi wrapper to simulate*

---

**Description**

The method `simulate` launches LibBi to simulate a model by passing ‘target="joint"’ to LibBi. If `x` is given as a ‘`bi_model`’, a [libbi](#) object will be created from the model.

**Usage**

```
## S3 method for class 'libbi'
simulate(x, ...)

## S3 method for class 'bi_model'
simulate(x, ...)
```

**Arguments**

`x` a [libbi](#) or [bi\\_model](#) object, or the name of a file containing the model  
`...` options to be passed to [run.libbi](#)

**Value**

a [bi\\_model](#) object

---

`summary`*Print summary information about a [libbi](#) object*

---

**Description**

This reads in the output file of the [libbi](#) object (which has been run before) and prints summary information of parameters.



**Usage**

```
## S3 method for class 'libbi'
summary(object, type = c("param", "state", "noise",
  "obs"), quantiles = c(0.25, 0.75), na.rm = FALSE, ...)
```

**Arguments**

object	a <code>libbi</code> object
type	one of "param" (default), "state", "noise" or "obs", the variable type to summarise
quantiles	quantiles to calculate (default: quartiles); minimum, median, mean and maximum are always calculated
na.rm	logical; if true, any na and NaN's are removed before calculations are performed
...	ignored

---

Unequals.bi_model	<i>Check if two models are unequal</i>
-------------------	--

---

**Description**

Ignores differences in the model name.

**Usage**

```
## S3 method for class 'bi_model'
e1 != e2
```

**Arguments**

e1	a <code>bi_model</code>
e2	a <code>bi_model</code>
...	ignored

**Value**

TRUE or FALSE

**Examples**

```
model_file_name <- system.file(package="rbi", "PZ.bi")
PZ <- bi_model(filename = model_file_name)
PZ != PZ # FALSE
```

---

update	<i>Update a libbi object</i>
--------	------------------------------

---

**Description**

This updates all the time stamps in a libbi object; it is useful after

**Usage**

```
## S3 method for class 'libbi'
update(x, ...)
```

**Arguments**

x	a <code>libbi</code> object
...	ignored

**Value**

a `libbi` object with updated timestamps

---

var_names	<i>Get variable names in a LibBi model</i>
-----------	--

---

**Description**

Get variable names of one or more type(s)

This returns all variable names of a certain type ("param", "state", "obs", "noise", "const") contained in the model of a `libbi` object

**Usage**

```
var_names(x, vars, type, dim = FALSE, opt = FALSE, aux = FALSE)
```

**Arguments**

x	a <code>bi_model</code> object
vars	a character vector of variable names; if given, only these variables names will be considered
type	a character vector of one or more types
dim	logical; if set to TRUE, names will contain dimensions in brackets
opt	logical; if set to TRUE, names will contain options (e.g., <code>has_output</code> )
aux	logical; if set to TRUE, auxiliary names will be returned

**Value**

variable names

---

write_model	<i>Writes a bi model to a file.</i>
-------------	-------------------------------------

---

### Description

Writes a bi model to a file given by filename. The extension '.bi' will be added if necessary.

### Usage

```
## S3 method for class 'bi_model'  
write_model(x, filename, update.name = TRUE, ...)  
  
## S3 method for class 'libbi'  
write_model(x, filename, ...)
```

### Arguments

x	a <a href="#">bi_model</a> object, or a <a href="#">libbi</a> object containing a model
filename	name of the file to be written
update.name	whether to update the model name with the file name
...	ignored

### Value

the return value of the [writeLines](#) call.

### See Also

[bi\\_model](#)

### Examples

```
model_file_name <- system.file(package="rbi", "PZ.bi")  
PZ <- bi_model(filename = model_file_name)  
write_model(PZ, "PZ.bi")
```

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